



PCT

RAW SEQUENCE LISTING

DATE: 10/17/2003

PATENT APPLICATION: US/10/070,560A

TIME: 14:50:30

Input Set : A:\Sequence.txt

Output Set: N:\CRF4\10172003\J070560A.raw

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3 <110> APPLICANT: Entremed, Inc.
 4 Liang, Hong
 5 Sim, Kim Lee
 6 Chang-Murad, Amy
 7 Zhou, Xinhua
 8 Madsen, John
 9 Boerner, Renee J.
 10 Bermejo, Lourdes L.
 11 Mistry, Firoz Rustom
 12 Shepard, Scott R.
 13 Schrimsher, Jeffrey L.
 15 <120> TITLE OF INVENTION: Method of Producing and Purifying Endostatin Protein
 17 <130> FILE REFERENCE: 05213-0551US (43170-258385)
 19 <140> CURRENT APPLICATION NUMBER: US 10/070,560A
 C--> 20 <141> **CURRENT FILING DATE: 2003-03-18**
 22 <150> PRIOR APPLICATION NUMBER: 60/153,698
 23 <151> PRIOR FILING DATE: 1999-09-14
 25 <150> PRIOR APPLICATION NUMBER: PCT/US00/25166
 26 <151> PRIOR FILING DATE: 2000-09-14
 28 <160> NUMBER OF SEQ ID NOS: 12
 30 <170> SOFTWARE: PatentIn version 3.1
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 33 <211> LENGTH: 35.
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Artificial Sequence
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: Synthetic primer
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 46 <212> TYPE: DNA
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 57 <211> LENGTH: 183
 58 <212> TYPE: PRT
 59 <213> ORGANISM: Homo sapiens
 61 <400> SEQUENCE: 3
 63 His Ser His Arg Asp Phe Gln Pro Val Leu His Leu Val Ala Leu Asn.

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68          20          25          30
71 Cys Phe Gln Gln Ala Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala
72          35          40          45
75 Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala
76          50          55          60
79 Asp Arg Ala Ala Val Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe
80 65          70          75          80
83 Pro Ser Trp Glu Ala Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro
84          85          90          95
87 Gly Ala Arg Ile Phe Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro
88          100          105          110
91 Thr Trp Pro Gln Lys Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg
92          115          120          125
95 Arg Leu Thr Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro Ser
96          130          135          140
99 Ala Thr Gly Gln Ala Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly Gln
100 145          150          155          160
103 Ser Ala Ala Ser Cys His His Ala Tyr Ile Val Leu Cys Ile Glu Asn
104          165          170          175
107 Ser Phe Met Thr Ala Ser Lys
108          180

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112 <211> LENGTH: 549

113 <212> TYPE: DNA

114 <213> ORGANISM: Homo sapiens

116 <400> SEQUENCE: 4

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121 gggctggcgg gcactttccg cgccttctctg tcctcgcgcc tgcaggacct gtacagcatc      180
123 gtgcgccgtg ccgaccgcgc agccgtgccc atcgtcaacc tcaaggacga gctgctgttt      240
125 cccagctggg aggctctgtt ctcaggctct gaggggtccgc tgaagcccgg ggcacgcac      300
127 ttctcctttg acggcaagga cgtcctgagg caccacacct ggccccagaa gagcgtgtgg      360
129 catggctcgg accccaacgg gcgcaggctg accgagagct actgtgagac gtggcggacg      420
131 gaggtccct cgccacggg ccaggcctcc tcgctgctgg ggggcaggct cctggggcag      480
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135 gcctccaag                                     549

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138 <210> SEQ ID NO: 5

139 <211> LENGTH: 182

140 <212> TYPE: PRT

141 <213> ORGANISM: Homo sapiens

143 <400> SEQUENCE: 5

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146 1          5          10          15
149 Ser Pro Leu Ser Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln
150          20          25          30
153 Cys Phe Gln Gln Ala Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala
154          35          40          45

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157 Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala
158      50                      55                      60
161 Asp Arg Ala Ala Val Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe
162 65                      70                      75                      80
165 Pro Ser Trp Glu Ala Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro
166                      85                      90                      95
169 Gly Ala Arg Ile Phe Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro
170                      100                     105                     110
173 Thr Trp Pro Gln Lys Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg
174                      115                     120                     125
177 Arg Leu Thr Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro Ser
178                      130                     135                     140
181 Ala Thr Gly Gln Ala Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly Gln
182 145                      150                     155                     160
185 Ser Ala Ala Ser Cys His His Ala Tyr Ile Val Leu Cys Ile Glu Asn
186                      165                     170                     175
189 Ser Phe Met Thr Ala Ser
190                      180
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194 <211> LENGTH: 181
195 <212> TYPE: PRT
196 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 6
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201 1                      5                      10                      15
204 Ser Pro Leu Ser Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln
205                      20                      25                      30
208 Cys Phe Gln Gln Ala Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala
209                      35                      40                      45
212 Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala
213      50                      55                      60
216 Asp Arg Ala Ala Val Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe
217 65                      70                      75                      80
220 Pro Ser Trp Glu Ala Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro
221                      85                      90                      95
224 Gly Ala Arg Ile Phe Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro
225                      100                     105                     110
228 Thr Trp Pro Gln Lys Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg
229                      115                     120                     125
232 Arg Leu Thr Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro Ser
233                      130                     135                     140
236 Ala Thr Gly Gln Ala Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly Gln
237 145                      150                     155                     160
240 Ser Ala Ala Ser Cys His His Ala Tyr Ile Val Leu Cys Ile Glu Asn
241                      165                     170                     175
244 Ser Phe Met Thr Ala
245                      180
248 <210> SEQ ID NO: 7
249 <211> LENGTH: 180

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250 <212> TYPE: PRT
251 <213> ORGANISM: Homo sapiens
253 <400> SEQUENCE: 7
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260 20 25 30
263 Cys Phe Gln Gln Ala Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala
264 35 40 45
267 Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala
268 50 55 60
271 Asp Arg Ala Ala Val Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe
272 65 70 75 80
275 Pro Ser Trp Glu Ala Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro
276 85 90 95
279 Gly Ala Arg Ile Phe Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro
280 100 105 110
283 Thr Trp Pro Gln Lys Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg
284 115 120 125
287 Arg Leu Thr Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro Ser
288 130 135 140
291 Ala Thr Gly Gln Ala Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly Gln
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314 Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln Cys Phe Gln Gln
315 20 25 30
318 Ala Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala Phe Leu Ser Ser
319 35 40 45
322 Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala Asp Arg Ala Ala
323 50 55 60
326 Val Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe Pro Ser Trp Glu
327 65 70 75 80
330 Ala Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro Gly Ala Arg Ile
331 85 90 95
334 Phe Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro Thr Trp Pro Gln
335 100 105 110
338 Lys Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg Arg Leu Thr Glu
339 115 120 125
342 Ser Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro Ser Ala Thr Gly Gln

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343      130      135      140
346 Ala Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly Gln Ser Ala Ala Ser
347 145      150      155      160
350 Cys His His Ala Tyr Ile Val Leu Cys Ile Glu Asn Ser Phe Met Thr
351      165      170      175
354 Ala Ser Lys
358 <210> SEQ ID NO: 9
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360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial Sequence
363 <220> FEATURE:
364 <223> OTHER INFORMATION: Synthetic primer
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380 accttccgcg ccttctgtgc ctgcgcctg caggacctgt acagcatcgt gcgccgtgcc      180
382 gaccgcgcag ccgtgcccac cgtcaacctc aaggacgagc tgctgtttcc cagctgggag      240
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386 ggcaaggacg tcctgaggca cccacactgg cccagaaga gcgtgtggca tggctcggac      360
388 cccaacgggc gcaggctgac cgagagctac tgtgagacgt ggcggaacgga ggctccctcg      420
390 gccacgggcc aggcctcctc gctgctgggg ggcaggctcc tggggcagag tgccgcgagc      480
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407      20      25      30
410 Ala Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala Phe Leu Ser Ser
411      35      40      45
414 Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala Asp Arg Ala Ala
415      50      55      60
418 Val Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe Pro Ser Trp Glu
419 65      70      75      80
422 Ala Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro Gly Ala Arg Ile
423      85      90      95
426 Phe Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro Thr Trp Pro Gln
427      100     105     110
430 Lys Ser Val Trp His Gly Ser Asp Pro Asn Gly Arg Arg Leu Thr Glu
431      115     120     125

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VERIFICATION SUMMARY

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Input Set : A:\Sequence.txt

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